49

SEQUENCE LISTING

<110>   Zamir, Dany
        Pleban, Tzili
        Fridman, Eyal

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AND USE OF SAME

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tatcctctat tttcaattta tgacaataat gctatgtttt tgctttcaaa a            13431
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<210>  2
<211>  20
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Single strand DNA oligonucleotide

<400>  2
tttgggctca ttcagtctca                                                20


<210>  3
<211>  18
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Single strand DNA oligonucleotide

<400>  3
aaattgttcg gcctcgtt                                                  18


<210>  4
<211>  3616
<212>  DNA
<213>  Lycopersicon pennellii

<400>  4
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tttataattt tatcaaacat taataggggca tttgcttctc ataatattttt tttggacttg   120

caatcttcaa gtgctattag tgtcaagaat gttcatagaa ctcgtttttca ttttcaacct   180
```

57

```
cctaaacatt ggattaatgg tatgttcatt ttttttttat tttatataac atgcgataaa   240
tttaacgtta gcaatgtggt ttgttattta aattcgaatt tgattatatg actttgctta   300
tataaatata catagtaata aaagtttgtg tataaatgca tgtcatatac atttattgac   360
ttggtatata tatcagtacg attaaattaa ttgatggtgc aattaatatt gcattattta   420
ggtgataaaa ctacagaaat taacgaaaat attttttta tatagagaag ttcaaatgtt   480
gagggttctt ttatggttac attggtttaa aatgtttttt gttaactatc tttatagcta   540
catatatata agagtgatca ttctttatat ttcaaaatta tatctacata cacacatata   600
catcattatg tggttcattt atggtagttt tcagtattcg atatttattt ttaagtttaa   660
tttatttaaa tctgcgttaa aatatctcac tttgaaagat agaatcactc ctgaccaact   720
atgagtaact cgattctcaa aattaaatt cggaattaga ttaattatca tggcaagaga   780
actaccacgt tttggataag aatgtgcaaa agagagaaag aaacatgaaa tatataaaaa   840
cctaagattt tggccatgga aagttaggtg cgaattaatt tgttgaaggc acccttat   900
attattatta taattattat tattattaat gaaatatagt gacattcat actcatatat   960
tgtgtgcatt taattaatat atgtagatct tatgttaatt taaacttacc aaacatattg  1020
tcttttataa agttgactcc cccctcaac cgccaacccc acccccaccc ccacccccacc  1080
caaaaaaaat acctcatcaa tttcggtttt tatatgactc aattttcttg tttaatttgt  1140
tatctacaga acggactact ttctatatca ttctacataa tatgtatatt ttttataatc  1200
caataaatct catgacacgt tttcagatca taatttgca aacacctttt tctttatttt  1260
ttaattaggt atatcacata aattaaaagg attcattaat tttcgcagag aaaactaatt  1320
agtttctgtg tttttcacct ttcatttatt aattactaca taattttaa tcaataattg  1380
atgaaagact atgtaatgta ttctattatc ttcactaatc attttttttt tgtataattc  1440
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gattattttt catttaattt tatcaataac tcaatgatat tattgatttt cattttatttt  1560
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ttcgtaaatg gatcaaacct aacaacaacc cgttgatcgt ccctgataac agtatcaata  1920
gaactgagtt tcgcgatcca actacagctt ggatggycca agatgggctt tggaggattt  1980
taatagcaag tatgagaaaa catagaggga tggcattgtt gtatagaagt agagatttta  2040
tgaaatggat caaagcccaa catccacttc attcatctac taatactgga aattgggagt  2100
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58

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gtcctgattt tttccctgta ttatttaata gtaccaatgg tttagatgta tcgtatcgcg    2160

gaaaaaatgt taaatatgtc ctcaagaata gtcttgatgt tgctaggttt gattattaca    2220

ctattggcat gtatcacacc aaaatagata ggtatattcc gaataacaat tcaattgatg    2280

gttggaaggg attgagaatc gactatggta atttctatgc atcgaagaca ttctatgatc    2340

ctagcagaaa tcgaagggtt atttggggtt ggtcaaatga atccgatgta ttacctgacg    2400

atgaaattaa gaaaggatgg gctggaattc aaggtattcc gcgacaagta tggctaaacc    2460

ttagtggtaa acaattactt caatggccta ttgaagaatt agaaacccta aggaagcaaa    2520

aggtccaatt gaacaacaag aagttgagca agggagaaat gtttgaagtt aaagggatct    2580

cagcatcaca ggtttcaact tttccttatt aaactatagt cttttaaata tcattaatct    2640

acttcttata tgtataatca atgtataact attatatcaa atgcacatga tcgattgatt    2700

atacatttgc tatatatata tctctattat atcaattgca ctgtctcatc ttgcatttct    2760

ttgatcgtag gctgatgttg aagtgctgtt ctcattttca agtttgaacg aggccgaaca    2820

atttgatcct agatgggctg acctatatgc ccaagacgtt tgtgccatta agggttcgac    2880

tatccaaggt gggcttggac catttgggct tgtgacatta gcttctaaaa acttagaaga    2940

atacacacct gttttcttcc gagtgttcaa ggctcaaaaa agttataaga ttctcatgtg    3000

ctcagatgct agaaggtttg tttcttcaat ccaattaatt gtaatgatcg aagttcacat    3060

cttctccaaa ttgagtaaat cgagaattat aatgacccga ctttgatatc atgataagaa    3120

atgcatttac ttatagatcg cccgttagtg tcattaaaaa actctaacct tgtttaggtt    3180

ttttttttttt ttaattaatg agcagatctt ccatgagaca aaatgaagca atgtacaagc    3240

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gtttggtaag ttttgctttc acaattttta tttatttata atttatttga tcaaaacttt    3360

caagattcga ttaatttgaa gagtaacgat ttgtgtttga ctaatcaatt tgtatcatat    3420

gcatatttt ttttagattg ataactcagt agtggaaagt ttcggtgctg gtggcaaaac    3480

atgcataaca tcaagggtgt atccaacttt agcgatttat gataatgcac atttatttgt    3540

ttttaacaat ggctctgaga caatcacaat tgagactctg aatgcttgga gcatggatgc    3600

atgtaagatg aactaa                                                     3616
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<210> 5
<211> 584
<212> PRT
<213> Lycopersicon pennellii

<400> 5

Met Glu Leu Phe Met Lys Asn Ser Ser Leu Trp Gly Leu Lys Phe Tyr
1   5   10   15

59

```
Leu Phe Cys Leu Phe Ile Ile Leu Ser Asn Ile Asn Arg Ala Phe Ala
            20              25              30

Ser His Asn Ile Phe Leu Asp Leu Gln Ser Ser Ser Ala Ile Ser Val
            35              40              45

Lys Asn Val His Arg Thr Arg Phe His Phe Gln Pro Pro Lys His Trp
            50              55              60

Ile Asn Asp Pro Asn Ala Pro Met Tyr Tyr Asn Gly Val Tyr His Leu
65              70              75                          80

Phe Tyr Gln Tyr Asn Pro Lys Gly Ser Val Trp Gly Asn Ile Ile Trp
                85              90              95

Ala His Ser Val Ser Lys Asp Leu Ile Asn Trp Ile His Leu Glu Pro
            100             105             110

Ala Ile Tyr Pro Ser Lys Lys Phe Asp Lys Tyr Gly Thr Trp Ser Gly
            115             120             125

Ser Ser Thr Ile Leu Pro Asn Asn Lys Pro Val Ile Ile Tyr Thr Gly
    130             135             140

Val Val Asp Ser Tyr Asn Asn Gln Val Gln Asn Tyr Ala Ile Pro Ala
145             150             155             160

Asn Leu Ser Asp Pro Phe Leu Arg Lys Trp Ile Lys Pro Asn Asn Asn
                165             170             175

Pro Leu Ile Val Pro Asp Asn Ser Ile Asn Arg Thr Glu Phe Arg Asp
            180             185             190

Pro Thr Thr Ala Trp Met Gly Gln Asp Gly Leu Trp Arg Ile Leu Ile
            195             200             205

Ala Ser Met Arg Lys His Arg Gly Met Ala Leu Leu Tyr Arg Ser Arg
    210             215             220

Asp Phe Met Lys Trp Ile Lys Ala Gln His Pro Leu His Ser Ser Thr
225             230             235             240

Asn Thr Gly Asn Trp Glu Cys Pro Asp Phe Phe Pro Val Leu Phe Asn
                245             250             255

Ser Thr Asn Gly Leu Asp Val Ser Tyr Arg Gly Lys Asn Val Lys Tyr
                260             265             270
```

```
                                        60
Val Leu Lys Asn Ser Leu Asp Val Ala Arg Phe Asp Tyr Tyr Thr Ile
        275             280             285

Gly Met Tyr His Thr Lys Ile Asp Arg Tyr Ile Pro Asn Asn Asn Ser
    290             295             300

Ile Asp Gly Trp Lys Gly Leu Arg Ile Asp Tyr Gly Asn Phe Tyr Ala
305             310             315             320

Ser Lys Thr Phe Tyr Asp Pro Ser Arg Asn Arg Arg Val Ile Trp Gly
                325             330             335

Trp Ser Asn Glu Ser Asp Val Leu Pro Asp Asp Glu Ile Lys Lys Gly
            340             345             350

Trp Ala Gly Ile Gln Gly Ile Pro Arg Gln Val Trp Leu Asn Leu Ser
        355             360             365

Gly Lys Gln Leu Leu Gln Trp Pro Ile Glu Glu Leu Glu Thr Leu Arg
    370             375             380

Lys Gln Lys Val Gln Leu Asn Asn Lys Lys Leu Ser Lys Gly Glu Met
385             390             395             400

Phe Glu Val Lys Gly Ile Ser Ala Ser Gln Ala Asp Val Glu Val Leu
            405             410             415

Phe Ser Phe Ser Ser Leu Asn Glu Ala Glu Gln Phe Asp Pro Arg Trp
            420             425             430

Ala Asp Leu Tyr Ala Gln Asp Val Cys Ala Ile Lys Gly Ser Thr Ile
        435             440             445

Gln Gly Gly Leu Gly Pro Phe Gly Leu Val Thr Leu Ala Ser Lys Asn
    450             455             460

Leu Glu Glu Tyr Thr Pro Val Phe Phe Arg Val Phe Lys Ala Gln Lys
465             470             475             480

Ser Tyr Lys Ile Leu Met Cys Ser Asp Ala Arg Arg Ser Ser Met Arg
            485             490             495

Gln Asn Glu Ala Met Tyr Lys Pro Ser Phe Ala Gly Tyr Val Asp Val
        500             505             510

Asp Leu Glu Asp Met Lys Lys Leu Ser Leu Arg Ser Leu Ile Asp Asn
    515             520             525
```

61

Ser Val Val Glu Ser Phe Gly Ala Gly Gly Lys Thr Cys Ile Thr Ser
    530   535   540

Arg Val Tyr Pro Thr Leu Ala Ile Tyr Asp Asn Ala His Leu Phe Val
545   550   555   560

Phe Asn Asn Gly Ser Glu Thr Ile Thr Ile Glu Thr Leu Asn Ala Trp
                565   570   575

Ser Met Asp Ala Cys Lys Met Asn
            580

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<210>  6
<211>  1960
<212>  DNA
<213>  Lycopersicon esculentum

<400>  6
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caatcttcaa gtgctattag tgtcaagaat gttcatagaa ctcgttttca ttttcaacct   180
cctaaacatt ggattaatga ccctaatgca ccaatgtatt ataatggagt gtatcattta   240
ttctatcaat acaatccaaa aggatcagta tggggcaata ttatttgggc tcattcagtc   300
tcaaaagact tgataaattg gatccattta gaacctgcaa tttatccatc caaaaaattt   360
gacaagtatg gtacttggtc tggatcatca actattttac ctaataacaa acctgttatc   420
atatacaccg gagtagtaga ttcgtataat aatcaagtcc agaactacgc catcccggct   480
aacctatctg atccatttct tcgtaaatgg atcaaaccta caacaaccc gttgatcgtc    540
cctgataaca gtatcaatag aactgagttt cgcgatccaa ctacagcttg gatgggccaa   600
gatgggcttt ggaggatttt aatagcaagt atgagaaaac atagagggat ggcattgttg   660
tatagaagta gagattttat gaaatggatc aaagcccaac atccacttca ttcatctact   720
aatactggaa attgggagtg tcctgatttt ttccctgtat tatttaatag taccaatggt   780
ttagatgtat cgtatcgcgg aaaaaatgtt aaatatgtcc tcaagaatag tcttgatgtt   840
gctaggtttg attattacac tattggcatg tatcacacca aaatagatag gtatattccg   900
aataacaatt caattgatgg ttggaaggga ttgagaatcg actatggtaa tttctatgca   960
tcgaagacat tctatgatcc tagcagaaat cgaagggtta tttggggttg gtcaaatgaa  1020
tccgatgtat tacctgacga tgaaattaag aaaggatggg ctggaattca aggtattccg  1080
cgacaagtat ggctaaacct tagtggtaaa caattacttc aatggcctat tgaagaatta  1140
gaaaccctaa ggagcaaaa ggtccaattg aacaacaaga agttgagcaa gggagaaatg  1200
tttgaagtta aagggatctc agcatcacag gctgatgttg aagtgctgtt ctcatttca  1260
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62

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agtttgaacg aggccgaaca atttgatcct agatgggctg acctatatgc ccaagacgtt   1320

tgtgccatta agggttcgac tatccaaggt gggcttggac catttgggct tgtgacatta   1380

gcttctaaaa acttagaaga atacacaccl gtttttcttcc gagtgttcaa ggctcaaaaa   1440

agttataaga ttctcatgtg ctcagatgct agaagatctt ccatgagaca aaatgaagca   1500

atgtacaagc cctcatttgc tggatatgta gatgtagatt tagaagacat gaagaagtta   1560

tctcttagga gtttgattga taactcagta gtggaaagtt tcggtgctgg tggcaaaaca   1620

tgcataacat caagggtgta tccaacttta gcgatttatg ataatgcaca tttatttgtt   1680

tttaacaatg gctctgagac aatcacaatt gagactctga atgcttggag catggatgca   1740

tgtaagatga actaaatatt ttcaaaaaaa ttggaattat gtctacaatt atatatgtct   1800

aaagagacaa aaattgtgtt aaattttaaca gtagatgatg ttcacaaaaa tcctctataa   1860

ttgtctctaa tttattttgg tgaatttaga aggcaaagtg tgtgtatgga tttttctagt   1920

accatatata tatatattaa gtaagaaatt tgttagcttt                          1960
```

<210> 7
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Beta-fructosidase motif

<400> 7

Asn Asp Pro Asn Gly
1   5

<210> 8
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Invertase catalytic motif

<400> 8

Trp Glu Cys Pro Asp Phe
1   5

<210> 9
<211> 500
<212> DNA
<213> Artificial sequence

<220>
<223> Sp9 marker probe

<400> 9
ttctgcaaga agataaaata atataatttt ttctagtaat ttaaatatta tatgtgaata   60

63

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tagacaaaat taaagggtat ttttggtacg acgtaaaaat aacttttttag aaaatatttt    180
tgcgagtata ttatttatta atgttttata ctaatataga agtcgttatt tttagggaaa    240
aaaagttctt ttcaaaatat gaaataaatt tctagcctag ggacgaaagt cttttttttt    300
tttataacta tagtaaacgt aaaatcacgt aattaaaaca ttataataa taaaagataa    360
aagatctata ttggttttac caattagtac atattaggtt ttagtcacgt taatatgttt    420
acttttttgt tctaatatta gtaattatct attaatcttg taatagctaa tttttttatt    480
tttttttgt aattgattaa                                                 500
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